

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.

Application Serial Number: 10/529,059  
Source: PCF  
Date Processed by STIC: 3/14/06

# ***ENTERED***



PCT

## RAW SEQUENCE LISTING

DATE: 03/14/2006

PATENT APPLICATION: US/10/529,059

TIME: 10:49:39

Input Set : A:\056646-5024-US Sequence Listing.txt

Output Set: N:\CRF4\03142006\J529059.raw

5 <110> APPLICANT: The University Court of the University of Glasgow  
 7 Stark, William M  
 9 Akopian, Aram  
 13 <120> TITLE OF INVENTION: Mutant Recombinases  
 17 <130> FILE REFERENCE: 056646-5024  
 20 <140> CURRENT APPLICATION NUMBER: US 10/529,059  
 C--> 22 <141> CURRENT FILING DATE: 2005-03-24  
 25 <150> PRIOR APPLICATION NUMBER: PCT/GB03/04169  
 27 <151> PRIOR FILING DATE: 2003-09-25  
 31 <150> PRIOR APPLICATION NUMBER: GE 0222229.7  
 33 <151> PRIOR FILING DATE: 2002-09-25  
 37 <160> NUMBER OF SEQ ID NOS: 32  
 41 <170> SOFTWARE: PatentIn version 3.1  
 45 <210> SEQ ID NO: 1  
 47 <211> LENGTH: 183  
 49 <212> TYPE: PRT  
 51 <213> ORGANISM: Escherichia coli  
 55 <400> SEQUENCE: 1  
 57 Met Arg Leu Phe Gly Tyr Ala Arg Val Ser Thr Ser Gln Gln Ser Leu  
 58 1 5 10 15  
 61 Asp Ile Gln Val Arg Ala Leu Lys Asp Ala Gly Val Lys Ala Asn Arg  
 62 20 25 30  
 65 Ile Phe Thr Asp Lys Ala Ser Gly Ser Ser Ser Asp Arg Lys Gly Leu  
 66 35 40 45  
 69 Asp Leu Leu Arg Met Lys Val Glu Glu Gly Asp Val Ile Leu Val Lys  
 70 50 55 60  
 73 Lys Leu Asp Arg Leu Gly Arg Asp Thr Ala Asp Met Ile Gln Leu Ile  
 74 65 70 75 80  
 77 Lys Glu Phe Asp Ala Gln Gly Val Ser Ile Arg Phe Ile Asp Asp Gly  
 78 85 90 95  
 81 Ile Ser Thr Asp Gly Glu Met Gly Lys Met Val Val Thr Ile Leu Ser  
 82 100 105 110  
 85 Ala Val Ala Gln Ala Glu Arg Gln Arg Ile Leu Glu Arg Thr Asn Glu  
 86 115 120 125  
 89 Gly Arg Gln Glu Ala Met Ala Lys Gly Val Val Phe Gly Arg Lys Arg  
 90 130 135 140  
 93 Lys Ile Asp Arg Asp Ala Val Leu Asn Met Trp Gln Gln Gly Leu Gly  
 94 145 150 155 160  
 97 Ala Ser His Ile Ser Lys Thr Met Asn Ile Ala Arg Ser Thr Val Tyr  
 98 165 170 175  
 101 Lys Val Ile Asn Glu Ser Asn  
 102 180  
 105 <210> SEQ ID NO: 2

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107 <211> LENGTH: 185
109 <212> TYPE: PRT
111 <213> ORGANISM: Escherichia coli
115 <400> SEQUENCE: 2
117 Met Arg Ile Phe Gly Tyr Ala Arg Val Ser Thr Ser Gln Gln Ser Leu
118 1 5 10 15
121 Asp Ile Gln Ile Arg Ala Leu Lys Asp Ala Gly Val Lys Ala Asn Arg
122 20 25 30
125 Ile Phe Thr Asp Lys Ala Ser Gly Ser Ser Thr Asp Arg Glu Gly Leu
126 35 40 45
129 Asp Leu Leu Arg Met Lys Val Glu Glu Gly Asp Val Ile Leu Val Lys
130 50 55 60
133 Lys Leu Asp Arg Leu Gly Arg Asp Thr Ala Asp Met Ile Gln Leu Ile
134 65 70 75 80
137 Lys Glu Phe Asp Ala Gln Gly Val Ala Val Arg Phe Ile Asp Asp Gly
138 85 90 95
141 Ile Ser Thr Asp Gly Asp Met Gly Gln Met Val Val Thr Ile Leu Ser
142 100 105 110
145 Ala Val Ala Gln Ala Glu Arg Arg Arg Ile Leu Glu Arg Thr Asn Glu
146 115 120 125
149 Gly Arg Gln Glu Ala Lys Leu Lys Gly Ile Lys Phe Gly Arg Arg Arg
150 130 135 140
153 Thr Val Asp Arg Asn Val Val Leu Thr Leu His Gln Lys Gly Thr Gly
154 145 150 155 160
157 Ala Thr Glu Ile Ala His Gln Leu Ser Ile Ala Arg Ser Thr Val Tyr
158 165 170 175
161 Lys Ile Leu Glu Asp Glu Arg Ala Ser
162 180 185
165 <210> SEQ ID NO: 3
167 <211> LENGTH: 186
169 <212> TYPE: PRT
171 <213> ORGANISM: Escherichia coli
175 <400> SEQUENCE: 3
177 Met Thr Gly Gln Arg Ile Gly Tyr Ile Arg Val Ser Thr Phe Asp Gln
178 1 5 10 15
181 Asn Pro Glu Arg Gln Leu Glu Gly Val Lys Val Asp Arg Ala Phe Ser
182 20 25 30
185 Asp Lys Ala Ser Gly Lys Asp Val Lys Arg Pro Gln Leu Glu Ala Leu
186 35 40 45
189 Ile Ser Phe Ala Arg Thr Gly Asp Thr Val Val Val His Ser Met Asp
190 50 55 60
193 Arg Leu Ala Arg Asn Leu Asp Asp Leu Arg Arg Ile Val Gln Thr Leu
194 65 70 75 80
197 Thr Gln Arg Gly Val His Ile Glu Phe Val Lys Glu His Leu Ser Phe
198 85 90 95
201 Thr Gly Glu Asp Ser Pro Met Ala Asn Leu Met Leu Ser Val Met Gly
202 100 105 110
205 Ala Phe Ala Glu Phe Glu Arg Ala Leu Ile Arg Glu Arg Gln Arg Glu
206 115 120 125

```

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209 Gly Ile Ala Leu Ala Lys Gln Arg Gly Ala Tyr Arg Gly Arg Lys Lys
210      130      135      140
213 Ser Leu Ser Ser Glu Arg Ile Ala Glu Leu Arg Gln Arg Val Glu Ala
214 145      150      155      160
217 Gly Glu Gln Lys Thr Lys Leu Ala Arg Glu Phe Gly Ile Ser Arg Glu
218      165      170      175
221 Thr Leu Tyr Gln Tyr Leu Arg Thr Asp Gln
222      180      185
225 <210> SEQ ID NO: 4
227 <211> LENGTH: 205
229 <212> TYPE: PRT
231 <213> ORGANISM: Streptococcus pyogenes
235 <400> SEQUENCE: 4
237 Met Ala Lys Ile Gly Tyr Ala Arg Val Ser Ser Lys Glu Gln Asn Leu
238 1      5      10      15
241 Asp Arg Gln Leu Gln Ala Leu Gln Gly Val Ser Lys Val Phe Ser Asp
242      20      25      30
245 Lys Leu Ser Gly Gln Ser Val Glu Arg Pro Gln Leu Gln Ala Met Leu
246      35      40      45
249 Asn Tyr Ile Arg Glu Gly Asp Ile Val Val Val Thr Glu Leu Asp Arg
250      50      55      60
253 Leu Gly Arg Asn Asn Lys Glu Leu Thr Glu Leu Met Asn Ala Ile Gln
254 65      70      75      80
257 Gln Lys Gly Ala Thr Leu Glu Val Leu Asn Leu Pro Ser Met Asn Gly
258      85      90      95
261 Ile Glu Asp Glu Asn Leu Arg Arg Leu Ile Asn Asn Leu Val Ile Glu
262      100      105      110
265 Leu Tyr Lys Tyr Gln Ala Glu Ser Glu Arg Lys Arg Ile Lys Glu Arg
266      115      120      125
269 Gln Ala Gln Gly Ile Glu Ile Ala Lys Ser Lys Gly Lys Phe Lys Gly
270      130      135      140
273 Arg Gln His Lys Phe Lys Glu Asn Asp Pro Arg Leu Lys His Ala Phe
274 145      150      155      160
277 Asp Leu Phe Leu Asn Gly Cys Ser Asp Lys Glu Val Glu Glu Gln Thr
278      165      170      175
281 Gly Ile Asn Arg Arg Thr Phe Arg Arg Tyr Arg Thr Arg Tyr Asn Val
282      180      185      190
285 Thr Val Asp Gln Arg Lys Asn Lys Gly Lys Arg Asp Ser
286      195      200      205
289 <210> SEQ ID NO: 5
291 <211> LENGTH: 202
293 <212> TYPE: PRT
295 <213> ORGANISM: Staphylococcus aureus
299 <400> SEQUENCE: 5
301 Met Ile Ile Gly Tyr Ala Arg Val Ser Ser Leu Asp Gln Asn Leu Glu
302 1      5      10      15
305 Arg Gln Leu Glu Asn Leu Lys Thr Phe Gly Ala Glu Lys Ile Phe Thr
306      20      25      30
309 Glu Lys Gln Ser Gly Lys Ser Ile Glu Asn Arg Pro Ile Leu Gln Lys

```

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```

310          35          40          45
313 Ala Leu Asn Phe Val Arg Met Gly Asp Arg Phe Ile Val Glu Ser Ile
314          50          55          60
317 Asp Arg Leu Gly Arg Asn Tyr Asn Glu Val Ile His Thr Val Asn Tyr
318 65          70          75          80
321 Leu Lys Asp Lys Glu Val Gln Leu Met Ile Thr Ser Leu Pro Met Met
322          85          90          95
325 Asn Glu Val Ile Gly Asn Pro Leu Leu Asp Lys Phe Met Lys Asp Leu
326          100         105         110
329 Ile Ile Gln Ile Leu Ala Met Val Ser Glu Gln Glu Arg Asn Glu Ser
330          115         120         125
333 Lys Arg Arg Gln Ala Gln Gly Ile Gln Val Ala Lys Glu Lys Gly Val
334          130         135         140
337 Tyr Lys Gly Arg Pro Leu Leu Tyr Ser Pro Asn Ala Lys Asp Pro Gln
338 145          150          155          160
341 Lys Arg Val Ile Tyr His Arg Val Val Glu Met Leu Glu Glu Gly Gln
342          165          170          175
345 Ala Ile Ser Lys Ile Ala Lys Glu Val Asn Ile Thr Arg Gln Thr Val
346          180          185          190
349 Tyr Arg Ile Lys His Asp Asn Gly Leu Ser
350          195          200
353 <210> SEQ ID NO: 6
355 <211> LENGTH: 201
357 <212> TYPE: PRT
359 <213> ORGANISM: Xanthomonas campestris
363 <400> SEQUENCE: 6
365 Met Lys Ile Gly Tyr Ala Arg Val Ser Thr Arg Glu Gln Asn Pro Ala
366 1          5          10          15
369 Leu Gln Val Asp Ser Leu Lys Ala Ala Gly Cys Glu Arg Ile Tyr Gln
370          20          25          30
373 Asp Val Ala Ser Gly Ala Lys Thr Ala Arg Pro Ala Leu Asp Glu Leu
374          35          40          45
377 Leu Gly Gln Leu Arg Gly Gly Asp Val Leu Val Ile Trp Lys Leu Asp
378          50          55          60
381 Arg Met Gly Arg Ser Leu Lys His Leu Val Glu Leu Val Gly Ser Leu
382 65          70          75          80
385 Met Glu Arg Lys Val Gly Leu Leu Ser Leu Asn Asp Pro Ile Asp Thr
386          85          90          95
389 Thr Ser Ala Gln Gly Arg Phe Val Phe Asn Leu Phe Ala Thr Leu Ala
390          100         105         110
393 Glu Phe Glu Arg Glu Leu Ile Arg Glu Arg Thr Gln Ala Gly Leu Thr
394          115         120         125
397 Ala Ala Arg Ala Arg Gly Arg Val Gly Gly Arg Pro Lys Gly Leu Ser
398          130         135         140
401 Pro Gln Ala Glu Ala Thr Ala Leu Ala Ala Glu Thr Leu Tyr Arg Glu
402 145          150          155          160
405 Arg Lys Leu Ser Val Ala Ala Ile Ala Gln Lys Leu His Leu Ser Lys
406          165          170          175
409 Ser Thr Leu Tyr Ser Tyr Leu Arg His Arg Gly Val Glu Ile Gly Pro

```

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```

410          180          185          190
413 Tyr Lys Gln Ser Ala Gln Ser Pro Ile
414          195          200
417 <210> SEQ ID NO: 7
419 <211> LENGTH: 193
421 <212> TYPE: PRT
423 <213> ORGANISM: Enterobacteria phage Mu
427 <400> SEQUENCE: 7
429 Met Leu Ile Gly Tyr Val Arg Val Ser Thr Asn Asp Gln Asn Thr Asp
430 1          5          10          15
433 Leu Gln Arg Asn Ala Leu Val Cys Ala Gly Cys Glu Gln Ile Phe Glu
434          20          25          30
437 Asp Lys Leu Ser Gly Thr Arg Thr Asp Arg Pro Gly Leu Lys Arg Ala
438          35          40          45
441 Leu Lys Arg Leu Gln Lys Gly Asp Thr Leu Val Val Trp Lys Leu Asp
442          50          55          60
445 Arg Leu Gly Arg Ser Met Lys His Leu Ile Ser Leu Val Gly Glu Leu
446 65          70          75          80
449 Arg Glu Arg Gly Ile Asn Phe Arg Ser Leu Thr Asp Ser Ile Asp Thr
450          85          90          95
453 Ser Ser Ala Met Gly Arg Phe Phe Phe His Val Met Gly Ala Leu Ala
454          100          105          110
457 Glu Met Glu Arg Glu Leu Ile Ile Glu Arg Thr Met Ala Gly Leu Ala
458          115          120          125
461 Ala Ala Arg Asn Lys Gly Arg Ile Gly Gly Arg Pro Pro Lys Leu Thr
462          130          135          140
465 Lys Ala Glu Trp Glu Gln Ala Gly Arg Leu Leu Ala Gln Gly Ile Pro
466 145          150          155          160
469 Arg Lys Gln Val Ala Leu Ile Tyr Asp Val Ala Leu Ser Thr Leu Tyr
470          165          170          175
473 Lys Lys His Pro Ala Lys Arg Ala His Ile Glu Asn Asp Asp Arg Ile
474          180          185          190
477 Asn
481 <210> SEQ ID NO: 8
483 <211> LENGTH: 190
485 <212> TYPE: PRT
487 <213> ORGANISM: Salmonella typhimurium
491 <400> SEQUENCE: 8
493 Met Ala Thr Ile Gly Tyr Ile Arg Val Ser Thr Ile Asp Gln Asn Ile
494 1          5          10          15
497 Asp Leu Gln Arg Asn Ala Leu Thr Ser Ala Asn Cys Asp Arg Ile Phe
498          20          25          30
501 Glu Asp Arg Ile Ser Gly Lys Ile Ala Asn Arg Pro Gly Leu Lys Arg
502          35          40          45
505 Ala Leu Lys Tyr Val Asn Lys Gly Asp Thr Leu Val Val Trp Lys Leu
506          50          55          60
509 Asp Arg Leu Gly Arg Ser Val Lys Asn Leu Val Ala Leu Ile Ser Glu
510 65          70          75          80
513 Leu His Glu Arg Gly Ala His Phe His Ser Leu Thr Asp Ser Ile Asp

```

## RAW SEQUENCE LISTING ERROR SUMMARY

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:32; Xaa Pos. 10

**VERIFICATION SUMMARY**

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L:22 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:1263 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32 after pos.:0